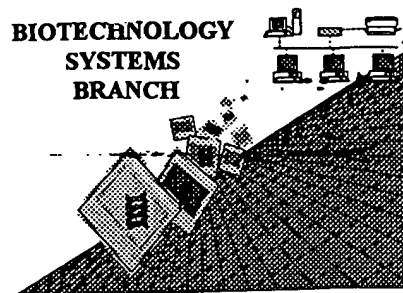


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/402,713
Source: ~~OTR~~ BATCH
Date Processed by STIC: 8/29/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October-1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/402713

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1643

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/402,713 DATE: 08/29/2000
 TIME: 16:50:53

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 Output Set : N:\CRF3\08292000\I402713.raw

Does Not Comply
 Corrected Diskette Needed

PP. 2-3,5

4 <110> APPLICANT: Bussemakers, Marion J.G.
 6 <120> TITLE OF INVENTION: PCA3, PCA3 Genes, and Methods of Use
 8 <130> FILE REFERENCE: 1619.0020001
 10 <140> CURRENT APPLICATION NUMBER: US 09/402,713
 C--> 11 <141> CURRENT FILING DATE: 2000-06-13
 13 <150> PRIOR APPLICATION NUMBER: PCT/CA98/00346
 14 <151> PRIOR FILING DATE: 1998-04-09
 16 <150> PRIOR APPLICATION NUMBER: US 60/041,836
 17 <151> PRIOR FILING DATE: 1997-04-10
 19 <160> NUMBER OF SEQ ID NOS: 8
 21 <170> SOFTWARE: PatentIn Ver. 2.1
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 40 tgtttcaatg aacaccaaga taaataagtg aagagctagt ccgctgtgag tctcctcagt 180
 42 gacacagggc tggatcacca tcgacggcac tttctgagta ctgagtgcag caaagaaaga 240
 44 ctacagacat ctcaatggca ggggtgagaa ataagaaagg ctgctgactt taccatctga 300
 46 gggccacacat ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata 360
 48 taatgtctaa gtagtgac atg ttt ttg cac att tcc agc ccc ttt aaa tat 411
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 50 1 5 10
 53 cca cac aca cag gaa gca caa aag gaa gca cag aga tcc ctg gga gaa 459
 54 Pro His Thr Gln Glu Ala Gln Lys Glu Ala Gln Arg Ser Leu Gly Glu
 55 15 20 25
 57 atg ccc ggc cgc cat ctt ggg tca tcg atg agc ctc gcc ctg tgc ctg 507
 58 Met Pro Gly Arg His Leu Gly Ser Ser Met Ser Leu Ala Leu Cys Leu
 59 30 35 40
 61 gtc ccg ctt gtg agg gaa gga cat tagaaaaatga attgatgtgt tccttaaagg 561
 62 Val Pro Leu Val Arg Glu Gly His
 63 45 50
 65 atgggcagga aaacagatcc tgttgtggat atttatttga acgggattac agatttgaaa 621
 67 tgaagtcaaa aagtgaagcat taccaatgag aggaaaacag acgagaaaat ctgtagggct 681
 69 tcacaagaca tgcaacaac aaatgggaat actgtgatga catgagggcag ccaagctggg 741
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 DATE: 08/29/2000
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 87 attccattaa tatcacagga ttaacttttt tttttaacct ggaagaattc aatgtttacat 1281
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 91 atccctcccc ttgtttgat tttttttcca gtataaagt aaaatgctta gccttgtaact 1401
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 103 aatgaagak ccacagaggg aatgtttatg gggcacgttt gtaagccttg gatgtgaagm 1761
 105 aaaggcaggg aacctcatag tatcttatat aatatacttc atttctctat ctctatcaca 1821
 107 atatccaaca agcttttcac agaattcatg cagtcaaat ccccaaaggt aacctttatc 1881
 109 catttcatgg tgagtgcgt ttagaatttt ggcaaatcat actggtcact tatctcaact 1941
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 126 Ala Gln Lys Glu Ala Gln Arg Ser Leu Gly Glu Met Pro Gly Arg His
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 149 agcaagatga caatataatg tctaagtagt gacatgtttt tgcacatttc cagccccttt 240
 150 aaatatccac acacacagga agcacaaaag gaagcacaga gatccctggg agaaatgcc 300
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 154 aatgagagga aaacagacga gaaaatcttg atggcttcac aagacatgca acaaacaaaa 540
 155 tggaaatactg tgatgacatg aggcagccaa gctggggagg agataaccac ggggcagagg 600

*see item 10 of
 Err Summary Sheet*

*insert the mandatory numeric identifier
 whenever a <221>
 <222>, or <223>
 numeric identifier
 is shown*

RAW SEQUENCE LISTING DATE: 08/29/2000
 PATENT APPLICATION: US/09/402,713 TIME: 16:50:53

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 157 taacctctaa aacaaagctg ttgtaataac tgatctctac gggttccttct gggcccaaca 720
 158 ttctccatat atccagccac actcattttt aatatttagt tccagatct gtactgtgac 780
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 175 aattttggca atcactatg gtcactttac tcaactttga gatgtgttg tccttgtagt 1800
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 197 aatgagagga aaacagacga gaaaatcttg atggcttcac aagacatgca acaaacaaaa 540
 198 tggataactg tgatgacatg aggcagccaa gctggggagg agataaccac ggggcagagg 600
 199 gtcaggatgc tggccctgct gcctaaactg tgcgttcata accaaatcat ttcatatattc 660
 200 taacctctaa aacaaagctg ttgtaataac tgatctctac gggttccttct gggcccaaca 720
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 210 <220> FEATURE:
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see item 10

RAW SEQUENCE LISTING DATE: 08/29/2000
 PATENT APPLICATION: US/09/402,713 TIME: 16:50:53

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236 gaattacaac acatatactt agtgtttcaa tgaacaccaa gataaataag tgaagagcta 180
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240 tactcagtgc agcaaagaaa gactacagac atctcaatgg caggggtgag aaataagaaa 300
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244 tagaaacagc aagatgacaa tataatgtct aagtagtgac atg ttt ttg cac att 415
245                                     Met Phe Leu His Ile
246                                     1             5
248 tcc agc ccc ttt aaa tat cca cac aca cag gaa gca caa aag gaa gca 463
249 Ser Ser Pro Phe Lys Tyr Pro His Thr Gln Glu Ala Gln Lys Glu Ala
250   10             15             20
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253 Gln Arg Ser Leu Gly Glu Met Pro Gly Arg His Leu Gly Ser Ser Met
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256 agc ctc gcc ctg tgc ctg gtc ccg ctt gtg agg gaa gga cat 553
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270 tcaaaacaaa gctgttgtaa tatctgatct ctacggttcc ttctggggcc aacattctcc 913
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354 cagtgtcttc tgcatctccc ctttctaata aagatccata gaatttgcta catttgagaa 3433
356 ttccaattag gaactcacat gttttatctg ccctatcaat tttttaaact tgctgaaaat 3493
358 taagtttttt caaaatctgt ccttgtaaat tactttttct tacagtgtct tggcatacta 3553
360 tatcaacttt gattctttgt tacaactttt

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363 <210> SEQ ID NO: 7

364 <211> LENGTH: 51

365 <212> TYPE: PRT

366 <213> ORGANISM: Unknown Organism

W--> 367 <220> FEATURE

367 <223> OTHER INFORMATION: Description of Unknown Organism: PCA3

369 <400> SEQUENCE: 7

370 Met Phe Leu His Ile Ser Ser Pro Phe Lys Tyr Pro His Thr Gln Glu

371 1 5 10 15

373 Ala Gln Lys Glu Ala Gln Arg Ser Leu Gly Glu Met Pro Gly Arg His

374 20 25 30

376 Leu Gly Ser Ser Met Ser Leu Ala Leu Cys Leu Val Pro Leu Val Arg

377 35 40 45

379 Glu Gly His

380 50

VERIFICATION SUMMARY

DATE: 08/29/2000

PATENT APPLICATION: US/09/402,713

TIME: 16:50:54

Input Set : A:\seqlist-1619 0020001.txt

Output Set: N:\CRF3\08292000\I402713.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:167 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:167 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:167 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:168 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:168 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:169 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:169 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:367 M:258 W: Mandatory Feature missing, <220> FEATURE: